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Asp Ile Ala Val Lys Ser Val Thr Leu Gly Ser Gly Gln Val Ser Ala
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Ala Ile Thr Ser Ser Thr Ser Ser Ala Ala Ser Leu Asn Asn Thr Asp
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Ser Ser Lys Lys Asn Thr Thr Ala Lys Leu Asn Lys Asp Ala Glu Asn
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8

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Asn Asn Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn
                 95                  100                 105

act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aac aca gaa  1588
Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu
         110                 115                 120

aac gat aat agt caa tta aag tta act aat aat gaa caa cca tca gcc  1636
Asn Asp Asn Ser Gln Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala
         125                 130                 135

gct act caa gca aac ttg aag aag cta aat cct caa gct gct aag gct  1684
Ala Thr Gln Ala Asn Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala
140                 145                 150                 155

gtt caa aat gcc aag att gat gcc ggt agt tta aca gat gat caa att  1732
Val Gln Asn Ala Lys Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile
                 160                 165                 170

aat gaa tta aat aag att aac ttc tct aag tct gct gaa aag ggt gca  1780
Asn Glu Leu Asn Lys Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala
             175                 180                 185

aaa ttg acc ttt aag gac tta gag ggg att ggt aat gct att gtt aag  1828
Lys Leu Thr Phe Lys Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys
         190                 195                 200

caa gat cca caa tat gct att cct tat tct aat gct aag gaa atc aag  1876
Gln Asp Pro Gln Tyr Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys
     205                 210                 215
```

```
aat atg cct gca aca tac act gta gat gcc caa aca ggt aag atg gct    1924
Asn Met Pro Ala Thr Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala
220             225             230             235

cat ctt gat gtc tgg gac tct tgg cca gta caa gat cct gtc aca ggt    1972
His Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly
                240             245             250

tat gta tct aat tac atg ggt tat caa cta gtt att gct atg atg ggt    2020
Tyr Val Ser Asn Tyr Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly
                255             260             265

att cca aat tcg cca act gga gat aat cat atc tat ctt ctt tac aac    2068
Ile Pro Asn Ser Pro Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn
                270             275             280

aag tat ggt gat aat gac ttt tct cat tgg cgc aat gca ggt tca atc    2116
Lys Tyr Gly Asp Asn Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile
        285             290             295

ttt gga act aaa gaa aca aat gtg ttc caa gaa tgg tca ggt tca gct    2164
Phe Gly Thr Lys Glu Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala
300             305             310             315

att gta aat gat gat ggt aca att caa cta ttt ttc acc tca aat gat    2212
Ile Val Asn Asp Asp Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp
                320             325             330

acg tct gat tac aag ttg aat gat caa cgc ctt gct acc gca aca tta    2260
Thr Ser Asp Tyr Lys Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu
                335             340             345

aac ctt aat gtt gat gat aac ggt gtt tca atc aag agt gtt gat aat    2308
Asn Leu Asn Val Asp Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn
                350             355             360

tat caa gtt ttg ttt gaa ggt gat gga ttt cac tac caa act tat gaa    2356
Tyr Gln Val Leu Phe Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu
        365             370             375

caa ttc gca aac ggc aaa gat cgt gaa aat gat gat tac tgc tta cgt    2404
Gln Phe Ala Asn Gly Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg
380             385             390             395

gac cca cac gtt gtt caa tta gaa aat ggt gat cgt tat ctt gta ttc    2452
Asp Pro His Val Val Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe
                400             405             410

gaa gct aat act ggg aca gaa gat tac caa agt gac gac caa att tat    2500
Glu Ala Asn Thr Gly Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr
                415             420             425

aat tgg gct aac tat ggt ggc gat gat gcc ttc aat att aag agt tcc    2548
Asn Trp Ala Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser
        430             435             440
```

11

```
ttc aag ctt ttg aat aat aag aag gat cgt gaa ttg gct ggt tta gct    2596
Phe Lys Leu Leu Asn Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala
    445             450             455

aat ggt gca ctt ggt atc tta aag ctc act aac aat caa agt aag cca    2644
Asn Gly Ala Leu Gly Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro
460             465             470             475

aag gtt gaa gaa gta tac tca cca ttg gta tct act ttg atg gct tgc    2692
Lys Val Glu Glu Val Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys
            480             485             490

gat gag gta nnn nnn aag ctt ggt gat aag tat tat ctc ttc tcc gta    2740
Asp Glu Val Xaa Xaa Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val
        495             500             505

act cgt gta agt cgt ggt tcc gat cgt gaa tta acc gct aag gat aac    2788
Thr Arg Val Ser Arg Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn
        510             515             520

aca atc gtt ggt gat aac gtt gct atg att ggt tac gtt tcc gat agc    2836
Thr Ile Val Gly Asp Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser
    525             530             535

tta atg ggt aag tac aag cca tta aat aac tca ggt gtc gta tta act    2884
Leu Met Gly Lys Tyr Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr
540             545             550             555

gca tca gta cct gca aac tgg cgt act gct act tat tcc tac tat gca    2932
Ala Ser Val Pro Ala Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala
            560             565             570

gta cct gta gct ggt cat cct gat caa gta tta att act tct tac atg    2980
Val Pro Val Ala Gly His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met
            575             580             585

agt aac aag gac ttt gct tca ggt gaa gga aac tat gca act tgg gca    3028
Ser Asn Lys Asp Phe Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala
            590             595             600

cca agt ttc tta gta caa atc aat cca gat gac acg aca act gta tta    3076
Pro Ser Phe Leu Val Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu
    605             610             615

gca cgt gca act aac caa ggt gac tgg gtg tgg gac gac tct agt cgg    3124
Ala Arg Ala Thr Asn Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg
620             625             630             635

aac gat aat atg ctc ggt gtt ctt aaa gaa ggt gca gct aac agt gcc    3172
Asn Asp Asn Met Leu Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala
            640             645             650

gcc tta cca ggt gaa tgg ggt aag cca gtt gac tgg agt ttg att aac    3220
Ala Leu Pro Gly Glu Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn
        655             660             665

aga agt cct ggc tta ggc tta aag cct cat caa cca gtt caa cca aag    3268
```

12

```
Arg Ser Pro Gly Leu Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys
        670               675               680

att gat caa cct gat caa caa cct tct ggt caa aac act aag aat gtc      3316
Ile Asp Gln Pro Asp Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val
        685               690               695

aca cca ggt aat ggt gat aag cct gct ggt aag gca act cct gat aac      3364
Thr Pro Gly Asn Gly Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn
700               705               710               715

act aat att gat cca agt gca caa cct tct ggt caa aac act aat att      3412
Thr Asn Ile Asp Pro Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile
                720               725               730

gat cca agt gca caa mct tct ggt caa aac act aag aat gtc aca cca      3460
Asp Pro Ser Ala Gln Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro
                735               740               745

ggt aat gag aaa caa ggt aag aat acc gat gca aaa caa tta cca caa      3508
Gly Asn Glu Lys Gln Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln
            750               755               760

aca ggt aat aag tct ggt tta gca gga ctt tac gct ggt tca tta ctt      3556
Thr Gly Asn Lys Ser Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu
        765               770               775

gcc ttg ttt gga ttg gca gca att gaa aag cgt cac gct taa            3598
Ala Leu Phe Gly Leu Ala Ala Ile Glu Lys Arg His Ala
780               785               790

tagagtaaaa aaacatcctc cactcaagtt acaagtagga taatatgtat tatttctacg 3658

cytagtcaag aggrattact ggacatannn nnnnnnnnnn tccagttacc aagtggaata 3718

tagtattatt ccacgctagt caggaggatt actgacatta ttggctacat ggccggtagt 3778

cctcttttct tttgtgacga attgtcaaac caagtgcaac ggtttctcaa aaaacacctc 3838

atatggggtt tcataattta acacttttcg aggacggcgg ttcagctgat gttggcagaa 3898

actgacgtcc ttatctgtat aatcatcaat attagccctt ttaggaaagt attccctaat 3958

tagsccattg gtattttcat tgggtcctct ttcctctggt gaatagggat ctggccaata 4018

gatagctact cctaaacgtc ctcgaatatc attcaagcca agaaattcac gcccatgatc 4078

tggagtcaat gaatggacaa attctttagg aatagaccct aagagatcaa ttaagccctg 4138

atatttgaat tcggagaagg ggagttgtcc aacaattgcc gttataatac cagggttaat 4198

acggccctgg gcctctacgg taatattgta tttttggctc agatcagtga tagaaaccca 4258

cagatttagc ttgccggtgg agtgctgctt gaagtcttca attacttcgt taccatgttt 4318

gattgctaat ctgatgtgtc gttgttgtgg tgtagtaggc atcataccac ctcctcataa 4378
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13

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aataaggtat aacaggaatt tcttgtacta tatgatcctt ccaatataat aatattaggc 4438

cgataagaaa tgaccagcta ccatttcttg atgcttagtg aatataatcg gatgatacgt 4498

cacccctcaa caatccaatt tcacggaggt gagtaatcat gccgagagct aggaatgatt 4558

ggaggaacga acacggtcca tgcggcagtg gctatttgga ttttagccaa agcagcgtta 4618

ctgcttgcaa aagctt                                                4634
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<212> PRT
<213> Lactobacillus reuteri

<400> 11

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Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala Thr Leu Val Ser Ala
 1               5                   10                  15

Ser Ile Leu Met Gly Gly Val Val Thr Ala His Ala Asp Gln Val Glu
            20                  25                  30

Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala
        35                  40                  45

Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn
    50                  55                  60

Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser Ala Thr Asn Asn Thr
65                  70                  75                  80

Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn
                85                  90                  95

Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Ala Val
            100                 105                 110

Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Asp Asn Ser Gln
        115                 120                 125

Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala Ala Thr Gln Ala Asn
    130                 135                 140

Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala Val Gln Asn Ala Lys
145                 150                 155                 160

Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile Asn Glu Leu Asn Lys
                165                 170                 175

Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala Lys Leu Thr Phe Lys
            180                 185                 190

Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys Gln Asp Pro Gln Tyr
        195                 200                 205

Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys Asn Met Pro Ala Thr
```

Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala His Leu Asp Val Trp
225   230   235   240

Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly Tyr Val Ser Asn Tyr
              245   250   255

Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly Ile Pro Asn Ser Pro
              260   265   270

Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn Lys Tyr Gly Asp Asn
              275   280   285

Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile Phe Gly Thr Lys Glu
       290   295   300

Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala Ile Val Asn Asp Asp
305   310   315   320

Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp Thr Ser Asp Tyr Lys
                 325   330   335

Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu Asn Leu Asn Val Asp
              340   345   350

Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn Tyr Gln Val Leu Phe
              355   360   365

Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu Gln Phe Ala Asn Gly
       370   375   380

Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg Asp Pro His Val Val
385   390   395   400

Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe Glu Ala Asn Thr Gly
              405   410   415

Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr Asn Trp Ala Asn Tyr
              420   425   430

Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser Phe Lys Leu Leu Asn
              435   440   445

Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala Asn Gly Ala Leu Gly
       450   455   460

Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro Lys Val Glu Glu Val
465   470   475   480

Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys Asp Glu Val Xaa Xaa
              485   490   495

Lys Leu Gly Asp Lys Tyr Tyr Leu Phe Ser Val Thr Arg Val Ser Arg
              500   505   510

Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn Thr Ile Val Gly Asp

Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser Leu Met Gly Lys Tyr
    530   535   540

Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr Ala Ser Val Pro Ala
545   550   555   560

Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Tyr Ala Val Pro Val Ala Gly
                565   570   575

His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met Ser Asn Lys Asp Phe
                580   585   590

Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala Pro Ser Phe Leu Val
                595   600   605

Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu Ala Arg Ala Thr Asn
    610   615   620

Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg Asn Asp Asn Met Leu
625   630   635   640

Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala Ala Leu Pro Gly Glu
                645   650   655

Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn Arg Ser Pro Gly Leu
                660   665   670

Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys Ile Asp Gln Pro Asp
                675   680   685

Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Gly
    690   695   700

Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn Thr Asn Ile Asp Pro
705   710   715   720

Ser Ala Gln Pro Ser Gly Gln Asn Thr Asn Ile Asp Pro Ser Ala Gln
                725   730   735

Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro Gly Asn Glu Lys Gln
                740   745   750

Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln Thr Gly Asn Lys Ser
    755   760   765

Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu Ala Leu Phe Gly Leu
    770   775   780

Ala Ala Ile Glu Lys Arg His Ala
785   790

<210> 12
<211> 24

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<212> DNA
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<220>
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<400> 12
ctgataataa tggaaatgta tcac                                    24


<210> 13
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 13
catgatcata agtttggtag taatag                                  26


<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 14
gtgatacatt tccattatta tcag                                    24


<210> 15
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

<400> 15
ctattactac caaacttatg atcatg                                  26


<210> 16
<211> 38
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<220>
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ccatggccat ggtagaacgc aaggaacata aaaaaatg                     38
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17

<210> 17
<211> 38
<212> DNA
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<220>
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agatctagat ctgttaaatc gacgtttgtt aatttctg   38

<210> 18
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<400> 18
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<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

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gtngcnswnc cnswccayts ytg   23

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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gaatgtaggt ccaatttttg gc   22

<210> 21
<211> 22
<212> DNA
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<400> 21
cctgtccgaa catcttgaac tg                                                    22


<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 22
arraanswng gngcvmangt nsw                                                   23


<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<400> 23
tayaayggng tngcngargt naa                                                   23


<210> 24
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence:primer

<400> 24
ccgaccatct tgtttgatta ac                                                    22


<210> 25
<211> 24
<212> DNA
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<220>
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<400> 25
aaytataayg gygttgcryg aagt                                                  24


<210> 26
<211> 21
<212> DNA
<213> Artificial Sequence
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taccgnwsnc tacttcaact t   21